AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph bridging pages 12 and 13 with the following amended paragraph:

To determine HPE genes and their expression, the invention, in one embodiment, provides a method wherein nucleic acid probes are immobilized on a substrate, such as a microchip, in an organized array (microarray). Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides (GeneChip® array, Affymetrix). These nucleic acid probes comprise a nucleotide sequence at least about 12 nucleotides in length, preferably at least about 15 nucleotides, more preferably at least about 25 nucleotides, and most preferably at least about 40 nucleotides, and up to all or nearly all of a sequence which is complementary to a portion of the coding sequence of one or more marker nucleic acid sequence.

Please replace the paragraph bridging pages 65 and 66 with the following amended paragraph:

In operation, the system 10 detects molecular interactions by measuring the spectral shift occurring at locations that are mapped to certain probes. Thus the substrate 12 may be a diffractive grating that is employed as a surface binding platform. When illuminated with white light, the substrate 12 is designed to reflect only a single wavelength. When molecules are attached to the surface, the reflected wavelength is shifted due to the change of the optical path of light that is coupled into the grating. Figure 2 depicts the substrate 12 having probes (reference numbers 20 and 22) attached to its surface. The probes can include actual probes and control probes. By linking probes or other receptor molecules to the surface of substrate 12, complementary binding molecules can be detected within the sample without the use of fluorescent probes or particle labels. It is understood that the detection technique is capable of resolving changes of ~0.1 nm thickness of protein binding, and can be performed with the grating surface either immersed in fluid or dried.

Please replace the paragraph at page 71, lines 15 through 26 with the following amended paragraph:

Table 1 summarizes the discriminatory genes obtained by applying the above procedure to the oral epithelium gene expression data. As an additional validation step of the experimental and

computational methods used in deriving these results, we selected three genes from Table 1 whose expressions are consistently altered in the 5 paired cases of oral cancer and applied real-time quantitative PCR (RT-QPCR) to independently measure their expression levels. The three genes were Neuromedin U (interacting protein with G-protein coupled receptors), Wilm's tumor related protein (tumor suppressor) and aldehyde dehydrogenase-10 (xenobiotic enzyme, fatty aldehyde dehydrogenase). Table 2 summarizes the RT-QPCR results of these three genes in the original 5 cases as well as 5 new independent cases of oral cancer. For the three genes identified, a positive comparison between the GeneChip® array expression data and RT-QPCR data is observed for more than 80% of the cases examined (3).

Please replace the paragraph at page 81, lines 1 through 5 with the following amended paragraph:

Table 2: Validation of 3 discriminatory genes (identified by GeneChip® array profiling and bioinformatic analysis) by real-time quantitative PCR (RT-QPCR). Shown are the numbers of cases where statistically significant differences between the control and malignant samples were found in the expression levels of the indicated genes using the two methods. GC= GeneChip® array data.